

SEQUENCE LISTING

<110> Presnell, Scott R.
Kindsvogel, Wayne

<120> NOVEL CYTOKINE ZCYT018

<130> 99-106

<150> US 60/172,105

<151> 1999-12-23

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<151> 2000-12-01

<160> 44

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (21)...(557)

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Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu

15 20 25

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac 149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp

30 35 40

002227 549460

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg 197
 Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu
 45 50 55

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att 245
 Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
 60 65 70 75

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg 293
 Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu
 80 85 90

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa 341
 Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
 95 100 105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389
 Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
 110 115 120

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437
 Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
 125 130 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
 His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
 140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
 Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
 160 165 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587
 Met Ser Leu Arg Asn Ala Cys Ile
 175

taacccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647
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 attttttaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887
 aaaccctaa atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat 947
 tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa 1007

09746375.12200

acatcattcg atattgctac ttgagtgtaa ggctaataatt gatatttatg acaataatta 1067
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<212> PRT

<213> Homo sapiens

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35 40 45
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
50 55 60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65 70 75 80
His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
85 90 95
Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
100 105 110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
115 120 125
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
130 135 140
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145 150 155 160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
165 170 175
Ala Cys Ile

<210> 3

<211> 167

<212> PRT

<213> Homo sapiens

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002222T"549460

Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala
 35 40 45
 Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly
 50 55 60
 Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met
 65 70 75 80
 Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser
 85 90 95
 Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg
 100 105 110
 Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His
 115 120 125
 Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly
 130 135 140
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 145 150 155 160
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 acnaaymgna cnttyatgyt ngcnaargar gcwnsnytn cngayaayaa yacngaygt 180
 mgnytnathg gngaraaryt nttycayggn gtnwsnatgw sngarmgntg ytayytnatg 240
 aarcargtny tnaayttyac nytnngargar gtnytnttyc cncarwsnga ymgnttycar 300
 ccntayatgc argargtngt nccnttyytn gcnmgnytnw snaaymgnyt nwsnacntgy 360
 cayathgarg gngaygayt ncayathcar mgnaaygtnc araarytnaa rgayacngtn 420
 aaraarytng gngarwsngg ngarathaar gcnathggng arytngayyt nytnttyatg 480
 wsnytnmgna aygcntgyat h 501

002221.5E9460

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 <223> Oligonucleotide primer ZC25840

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 <223> Oligonucleotide primer ZC25841

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<210> 7
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<210> 9
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<400> 11
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<210> 12
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<220>
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<400> 12

002227" 549460

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18

<210> 13

<211> 18

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<223> Oligonucleotide primer ZC26415

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<210> 14

<211> 6

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<213> Artificial Sequence

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<223> Glu-Glu (CEE) peptide Tag amino acid sequence

<400> 14

Glu Tyr Met Pro Met Glu

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<213> Artificial Sequence

<220>

<223> C-terminal FLAG peptide tag

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5

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<212> DNA

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<223> Oligonucleotide primer ZC28590

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<210> 17

<211> 33

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<222> (34)...(1755)

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Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
10 15 20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
25 30 35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
40 45 50 55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt 246

0022215-122200

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cag	cgg	atc	acc	cgg	aag	tcc	tgc	aac	ctg	acg	gtg	gag	acg	ggc	aac	294
Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu	Thr	Val	Glu	Thr	Gly	Asn	
			75					80						85		
ctc	acg	gag	ctc	tac	tat	gcc	agg	gtc	acc	gct	gtc	agt	gcg	gga	ggc	342
Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr	Ala	Val	Ser	Ala	Gly	Gly	
			90				95						100			
cgg	tca	gcc	acc	aag	atg	act	gac	agg	ttc	agc	tct	ctg	cag	cac	act	390
Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	
	105					110					115					
acc	ctc	aag	cca	cct	gat	gtg	acc	tgt	atc	tcc	aaa	gtg	aga	tcg	att	438
Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	
	120				125					130					135	
cag	atg	att	gtt	cat	cct	acc	ccc	acg	cca	atc	cgt	gca	ggc	gat	ggc	486
Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly	
				140				145						150		
cac	cgg	cta	acc	ctg	gaa	gac	atc	ttc	cat	gac	ctg	ttc	tac	cac	tta	534
His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu	
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gag	ctc	cag	gtc	aac	cgc	acc	tac	caa	atg	cac	ctt	gga	ggg	aag	cag	582
Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln	
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Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro	Asp	Thr	Glu	Phe	Leu	Gly	
	185					190					195					
acc	atc	atg	att	tgc	gtt	ccc	acc	tgg	gcc	aag	gag	agt	gcc	ccc	tac	678
Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala	Lys	Glu	Ser	Ala	Pro	Tyr	
	200				205					210					215	
atg	tgc	cga	gtg	aag	aca	ctg	cca	gac	cgg	aca	tgg	acc	tac	tcc	ttc	726
Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg	Thr	Trp	Thr	Tyr	Ser	Phe	
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tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc	774
Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	
235 240 245	
tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc	822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser	
250 255 260	
ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag	870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln	
265 270 275	
gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg	918
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu	
280 285 290 295	
gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag	966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu	
300 305 310	
ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta	1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu	
315 320 325	
ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc	1062
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	
330 335 340	
cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc	1110
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val	
345 350 355	
ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca	1158
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	
360 365 370 375	
ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc	1206
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
380 385 390	
cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg	1254
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	
395 400 405	

gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa	1302
Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys	
410 415 420	
cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc	1350
His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser	
425 430 435	
tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg	1398
Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	
440 445 450 455	
gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc	1446
Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys	
460 465 470	
aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg	1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly	
475 480 485	
aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag	1542
Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln	
490 495 500	
atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca	1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	
505 510 515	
tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc	1638
Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser	
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ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca	1686
Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser	
540 545 550	
gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc	1734
Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala	
555 560 565	
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002221" 52694260

Leu Thr Val Gln Trp Glu Ser
570

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<213> Homo sapiens

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Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp
	50					55				60					
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn
65					70				75					80	
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val
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09746375.122200

Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
 115 120 125
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
 130 135 140
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 165 170 175
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 180 185 190
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
 225 230 235 240
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
 245 250 255
 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
 260 265 270
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
 275 280 285
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
 290 295 300
 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
 305 310 315 320
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
 325 330 335
 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
 340 345 350
 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
 355 360 365
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
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 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
 385 390 395 400
 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
 405 410 415
 Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
 420 425 430
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
 435 440 445

09746375.122200

Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
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 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 465 470 475 480
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 485 490 495
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
 500 505 510
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
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37

<210> 22

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<223> Oligonucleotide primer ZC25963

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 1 5 10 15

act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag 96
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag 144
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
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cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac 192

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aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt	240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	
65 70 75 80	
act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag	288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	
85 90 95	
gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca	336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	
100 105 110	
gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata	384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	
115 120 125	
gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta	432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	
130 135 140	
att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat	480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	
145 150 155 160	
gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att	528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	
165 170 175	
aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga	576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	
180 185 190	
gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg	624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	
195 200 205	
gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa	672
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu	
210 215 220	

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 Glu Arg Cys Val Glu Ile Pro
 225 230

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 35 40 45
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

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Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220
 Glu Arg Cys Val Glu Ile Pro
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<213> Artificial Sequence

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<223> Human ZCYT018 peptide 1 (huZCYT018-1)

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 Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys
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<212> PRT

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<223> Human ZCYT018 peptide 2 (huZCYT018-2)

<400> 35

Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro Tyr Met Gln
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 Glu Val Val Pro Cys
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<210> 36

<211> 24

<212> PRT

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<223> Human ZCYT018 peptide 3 (huZCYT018-3)

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 Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu Ala Ala Ser
 5 10 15

tgc ctg ctt ctc att gcc ctg tgg gcc cag gag gca aat gcg ctg ccc 151
 Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn Ala Leu Pro
 20 25 30 35

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gtc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag cag ccg tac 199
 Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln Pro Tyr
 40 45 50

atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc ctt gca gat 247
 Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu Ala Asp
 55 60 65

aac aac aca gat gtc cgg ctc atc ggg gag aaa ctg ttc cga gga gtc 295
 Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg Gly Val
 70 75 80

aat gct aag gat cag tgc tac ctg atg aag cag gtg ctc aac ttc acc 343
 Asn Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn Phe Thr
 85 90 95

ctg gaa gac gtt ctg ctc ccc cag tca gac agg ttc cag ccc tac atg 391
 Leu Glu Asp Val Leu Leu Pro Gln Ser Asp Arg Phe Gln Pro Tyr Met
 100 105 110 115

cag gag gtg gtg cct ttc ctg acc aaa ctc agc aat cag ctc agc tcc 439
 Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu Ser Ser
 120 125 130

tgt cac atc agc ggt gac gac cag aac atc cag aag aat gtc aga agg 487
 Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val Arg Arg
 135 140 145

ctg aag gag aca gtg aaa aag ctt gga gag agt gga gag atc aag gcg 535
 Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala
 150 155 160

att ggg gaa ctg gac ctg ctg ttt atg tct ctg aga aat gct tgc gtc 583
 Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Val
 165 170 175

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 aagatccctg aatggacttt ttactaaag gaaagtgaga agctaacgtc catcatcatt 703
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 <213> mus musculus

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 Ala Leu Pro Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
 35 40 45
 Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65 70 75 80
 Arg Gly Val Asn Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Asp Val Leu Leu Pro Gln Ser Asp Arg Phe Gln
 100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln
 115 120 125
 Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn
 130 135 140
 Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
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 Ala Cys Val

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<210> 40
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<223> Oligonucleotide primer ZC37126

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32

<210> 41

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<210> 42

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC28345

<400> 42

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28

<210> 43

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC447

<400> 43

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17

<210> 44

<211> 18

002222 " 5/2E94/60

<212> DNA

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<223> Oligonucleotide primer ZC976

<400> 44

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